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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	Coyle, Anthony J. et al.		
Application No.:	10/644,671	Group No.:	1644
Filed:	August 20, 2003	Examiner:	Ouspenski, Ilia I.
For:	SCREENING METHODS USING B7-H2 MOLECULES, MEMBERS OF THE B7 FAMILY (as amended)		

Mail Stop Amendment
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

AMENDMENT AND RESPONSE

Sir: In response to the Office action mailed June 21, 2006, entry and consideration of the following remarks and amendments is requested:

Amendments to the Specification begin on page 2 of this paper.

Amendments to the Claims are reflected in the listing of claims which begins on page 3 of this paper.

Remarks/Arguments begin on page 5 of this paper.

CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10*

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IN THE SPECIFICATION:

At page 1 of the specification, please amend the title as follows:

SCREENING METHODS USING B7-H2 MOLECULES, ~~NOVEL~~ MEMBERS OF THE B7
FAMILY
~~AND USES THEREOF~~

At pages 24-25 of the specification, please amend the paragraph beginning at page 24, line 12, as follows:

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, nonlimiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to B7-like nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to B7-like protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-Blast can be used to perform an iterated search that detects distant relationships between molecules. *See* Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. ~~*See* www.ncbi.nlm.nih.gov.~~ Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0), which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

At page 97 of the specification, please amend the title of the abstract as follows:

SCREENING METHODS USING B7-H2 MOLECULES, ~~NOVEL~~ MEMBERS OF THE B7
FAMILY
~~AND USES THEREOF~~